

SEQUENCE LISTING

<110> SOLVAY PHARMACEUTICALS B.V.

<120> Novel human G-protein coupled receptor

<130> SPW99.04

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<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 1659

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (36)..(1559)

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Asn Ser Thr Arg Glu Ser Asn Ser His Thr Cys Met Pro Leu Ser
10 15 20

aaa atg ccc atc agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg 149
Lys Met Pro Ile Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu
25 30 35

gtt atc ttc ctc gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta 197
Val Ile Phe Leu Ala Ala Ser Phe Val Gly Asn Ile Val Leu Ala Leu
40 45 50

gtg ttg cag cgc aag ccg cag ctg ctg cag gtg acc aac cgt ttt atc 245
Val Leu Gln Arg Lys Pro Gln Leu Leu Gln Val Thr Asn Arg Phe Ile
55 60 65 70

ttt aac ctc ctc gtc acc gac ctg ctg cag att tcg ctc gtg gcc ccc 293
Phe Asn Leu Leu Val Thr Asp Leu Leu Gln Ile Ser Leu Val Ala Pro
75 80 85

tgg gtg gtg gcc acc tct gtg cct ctc ttc tgg ccc ctc aac agc cac 341
Trp Val Val Ala Thr Ser Val Pro Leu Phe Trp Pro Leu Asn Ser His
90 95 100

ttc tgc acg gcc ctg gtt agc ctc acc cac ctg ttc gcc ttc gcc agc 389
Phe Cys Thr Ala Leu Val Ser Leu Thr His Leu Phe Ala Phe Ala Ser
105 110 115

a4

gtc aac acc att gtc ttg gtg tca gtg gat cgc tac ttg tcc atc atc 437
 Val Asn Thr Ile Val Leu Val Ser Val Asp Arg Tyr Leu Ser Ile Ile
 120 125 130

cac cct ctc tcc tac ccg tcc aag atg acc cag cgc cgc ggt tac ctg 485
 His Pro Leu Ser Tyr Pro Ser Lys Met Thr Gln Arg Arg Gly Tyr Leu
 135 140 145 150

ctc ctc tat ggc acc tgg att gtg gcc atc ctg cag agc act cct cca 533
 Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile Leu Gln Ser Thr Pro Pro
 155 160 165

ctc tac ggc tgg ggc cag gct gcc ttt gat gag cgc aat gct ctc tgc 581
 Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp Glu Arg Asn Ala Leu Cys
 170 175 180

tcc atg atc tgg ggg gcc agc ccc agc tac act att ctc agc gtg gtg 629
 Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr Thr Ile Leu Ser Val Val
 185 190 195

tcc ttc atc gtc att cca ctg att gtc atg att gcc tgc tac tcc gtg 677
 Ser Phe Ile Val Ile Pro Leu Ile Val Met Ile Ala Cys Tyr Ser Val
 200 205 210

gtg ttc tgt gca gcc cg^a agg cag cat gct ctg tac aat gtc aag 725
 Val Phe Cys Ala Ala Arg Arg Gln His Ala Leu Leu Tyr Asn Val Lys
 215 220 225 230

aga cac agc ttg gaa gtg cga gtc aag gac tgt gtg gag aat gag gat 773
 Arg His Ser Leu Glu Val Arg Val Lys Asp Cys Val Glu Asn Glu Asp
 235 240 245

gaa gag gga gca gag aag aag gag gag ttc cag gat gag agt gag ttt 821
 Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe Gln Asp Glu Ser Glu Phe
 250 255 260

cgc cgc cag cat gaa ggt gag gtc aag gcc aag gag ggc aga atg gaa 869
 Arg Arg Gln His Glu Gly Glu Val Lys Ala Lys Glu Gly Arg Met Glu
 265 270 275

gcc aag gac ggc agc ctg aag gcc aag gaa gga agc acg ggg acc agt 917
 Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu Gly Ser Thr Gly Thr Ser
 280 285 290

gag agt agt gta gag gcc agg ggc agc gag gag gtc aga gag agc agc 965
 Glu Ser Ser Val Glu Ala Arg Gly Ser Glu Glu Val Arg Glu Ser Ser
 295 300 305 310

acg gtg gcc agc gac ggc agc atg gag ggt aag gaa ggc agc acc aaa 1013
 Thr Val Ala Ser Asp Gly Ser Met Glu Gly Lys Glu Gly Ser Thr Lys
 315 320 325

gtt gag gag aac agc atg aag gca gac aag ggt cgc aca gag gtc aac 1061
 Val Glu Glu Asn Ser Met Lys Ala Asp Lys Gly Arg Thr Glu Val Asn
 330 335 340

cag tgc agc att gac ttg ggt gaa gat ggc atg gag ttt ggt gaa gac 1109

At
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Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly Met Glu Phe Gly Glu Asp
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gac atc aat ttc agt gag gat gac gtc gag gca gtg aac atc ccg gag 1157
 Asp Ile Asn Phe Ser Glu Asp Asp Val Glu Ala Val Asn Ile Pro Glu
 360 365 370

agc ctc cca ccc agt cgt cgt aac agc aac agc aac cct cct ctg ccc 1205
 Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn Ser Asn Pro Pro Leu Pro
 375 380 385 390

agg tgc tac cag tgc aaa gct gct aaa gtg atc ttc atc atc att ttc 1253
 Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val Ile Phe Ile Ile Ile Phe
 395 400 405

tcc tat gtg cta tcc ctg ggg ccc tac tgc ttt tta gca gtc ctg gcc 1301
 Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys Phe Leu Ala Val Leu Ala
 410 415 420

gtg tgg gtg gat gtc gaa acc cag gta ccc cag tgg gtg atc acc ata 1349
 Val Trp Val Asp Val Glu Thr Gln Val Pro Gln Trp Val Ile Thr Ile
 425 430 435

atc atc tgg ctt ttc ctg cag tgc tgc atc cac ccc tat gtc tat 1397
 Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys Ile His Pro Tyr Val Tyr
 440 445 450

ggc tac atg cac aag acc att aag aag gaa atc cag gac atg ctg aag 1445
 Gly Tyr Met His Lys Thr Ile Lys Lys Glu Ile Gln Asp Met Leu Lys
 455 460 465 470

aag ttc ttc tgc aag gaa aag ccc ccg aaa gaa gat agc cac cca gac 1493
 Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys Glu Asp Ser His Pro Asp
 475 480 485

ctg ccc gga aca gag ggt ggg act gaa ggc aag att gtc cct tcc tac 1541
 Leu Pro Gly Thr Glu Gly Thr Glu Gly Lys Ile Val Pro Ser Tyr
 490 495 500

gat tct gct act ttt cct tgaaggtagt tctaaggcaa accttgaaaa 1589
 Asp Ser Ala Thr Phe Pro
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gctttctgtg 1659

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35 40 45

Asn Ile Val Leu Ala Leu Val Leu Gln Arg Lys Pro Gln Leu Leu Gln
50 55 60

Val Thr Asn Arg Phe Ile Phe Asn Leu Leu Val Thr Asp Leu Leu Gln
65 70 75 80

Ile Ser Leu Val Ala Pro Trp Val Val Ala Thr Ser Val Pro Leu Phe
85 90 95

Trp Pro Leu Asn Ser His Phe Cys Thr Ala Leu Val Ser Leu Thr His
100 105 110

Leu Phe Ala Phe Ala Ser Val Asn Thr Ile Val Leu Val Ser Val Asp
115 120 125

Arg Tyr Leu Ser Ile Ile His Pro Leu Ser Tyr Pro Ser Lys Met Thr
130 135 140

Gln Arg Arg Gly Tyr Leu Leu Tyr Gly Thr Trp Ile Val Ala Ile
145 150 155 160

Leu Gln Ser Thr Pro Pro Leu Tyr Gly Trp Gly Gln Ala Ala Phe Asp
165 170 175

Glu Arg Asn Ala Leu Cys Ser Met Ile Trp Gly Ala Ser Pro Ser Tyr
180 185 190

Thr Ile Leu Ser Val Val Ser Phe Ile Val Ile Pro Leu Ile Val Met
195 200 205

Ile Ala Cys Tyr Ser Val Val Phe Cys Ala Ala Arg Arg Gln His Ala
210 215 220

Leu Leu Tyr Asn Val Lys Arg His Ser Leu Glu Val Arg Val Lys Asp
225 230 235 240

Cys Val Glu Asn Glu Asp Glu Glu Gly Ala Glu Lys Lys Glu Glu Phe
245 250 255

Gln Asp Glu Ser Glu Phe Arg Arg Gln His Glu Gly Glu Val Lys Ala
260 265 270

Lys Glu Gly Arg Met Glu Ala Lys Asp Gly Ser Leu Lys Ala Lys Glu
275 280 285

Gly Ser Thr Gly Thr Ser Glu Ser Ser Val Glu Ala Arg Gly Ser Glu
290 295 300

Glu Val Arg Glu Ser Ser Thr Val Ala Ser Asp Gly Ser Met Glu Gly
305 310 315 320

A
4
cont

Lys Glu Gly Ser Thr Lys Val Glu Glu Asn Ser Met Lys Ala Asp Lys
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Gly Arg Thr Glu Val Asn Gln Cys Ser Ile Asp Leu Gly Glu Asp Gly
340 345 350

Met Glu Phe Gly Glu Asp Asp Ile Asn Phe Ser Glu Asp Asp Val Glu
355 360 365

Ala Val Asn Ile Pro Glu Ser Leu Pro Pro Ser Arg Arg Asn Ser Asn
370 375 380

Ser Asn Pro Pro Leu Pro Arg Cys Tyr Gln Cys Lys Ala Ala Lys Val
385 390 395 400

Ile Phe Ile Ile Ile Phe Ser Tyr Val Leu Ser Leu Gly Pro Tyr Cys
405 410 415

Phe Leu Ala Val Leu Ala Val Trp Val Asp Val Glu Thr Gln Val Pro
420 425 430

Gln Trp Val Ile Thr Ile Ile Trp Leu Phe Phe Leu Gln Cys Cys
435 440 445

Ile His Pro Tyr Val Tyr Gly Tyr Met His Lys Thr Ile Lys Lys Glu
450 455 460

Ile Gln Asp Met Leu Lys Lys Phe Phe Cys Lys Glu Lys Pro Pro Lys
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<400> 13
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<211> 25
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25

A^Y

✓

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